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On page 6, lines 4-6, please replace the original paragraph with the following paragraph.

CZ

Figure 1 shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a differentially expressed protein provides herein, CHA4.

On page 11, lines 9-19 please substitute the existing paragraph with the following paragraph:

C3

In a preferred embodiment, differentially expressed sequences are those that are up-regulated in breast cancer and/or colorectal cancer; that is, the expression of these genes is higher in carcinoma as compared to normal breast or colon tissue. "Up-regulation as used herein means at least about a 50% increase, preferably a two-fold change, more preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see e.g., Benson, DA et al., Nucleic Acids Research 26:1-7 (1998). In addition, these genes were found to be expressed in a limited amount or not at all in heart, brain, lung, liver, kidney, muscle, pancreas, testes, stomach, small intestine and spleen.

On page 15, lines 17-30 please replace the existing paragraph with the following paragraph:

C4

Another example of a useful algorithm is the BLAST algorithm, described in Atschul et al., J. Mol. Biol. 215, 403-410 (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Atschul et al., Methods in Enzymology, 266:460-480 (1996). WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2

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parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and the composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-BLAST-2 to maximize the alignment score are ignored).

~~Please change the title of the application to:~~ Novel Methods for Diagnosis and Prognosis Evaluation of Colorectal Cancer and/or Breast Cancer.

IN THE CLAIMS:

Please cancel claims 36 and 40. Please add claims 48, 49, 50, and 51. Please amend claims 32, 34, 35, 38, 39, 41, 44, and 45 as follows.

32.   (Amended) A method of diagnosing breast cancer or colorectal cancer comprising:

a) determining the expression of a nucleic acid that encodes an amino acid sequence at least 95% identical to SEQ ID NO:2. in a first sample of a first individual; and

b) comparing the expression of said nucleic acid in the first sample to expression of said nucleic acid in a second sample; wherein an increase in expression of said nucleic acid in the first sample relative to the second sample provides a diagnosis of breast cancer or colorectal cancer in the first individual.

34.   (Amended) The method of claim 33, wherein said first sample is colorectal tissue.